

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claim 1 (original): Method for improving plant growth characteristics selected from one or more of increased yield, increased growth rate and modified architecture, said method comprising increasing expression in a plant of a nucleic acid encoding a B-type CDK protein and/or increasing activity and/or levels in a plant of a B-type CDK protein.

Claim 2 (original): Method according to claim 1, wherein said increasing expression is effected by introducing and expressing in a plant a B-type CDK nucleic acid.

Claim 3 (original): Method according to claim 1 or 2, wherein said B-type CDK is derived from a plant, algal or fungal source.

Claim 4 (original): Method according to claim 3, wherein said B-type CDK derived from a plant is preferably from a dicotyledonous plant, further preferably from the family *Brassicaceae*, more preferably the nucleic acid sequence is from *Arabidopsis thaliana*.

Claim 5 (currently amended): Method according to ~~any one of claims 1 to 4~~ claim 3, wherein said B-type CDK is a class 1 B-type CDK, preferably a CDK B1;1 from *Arabidopsis thaliana* or a CDK B1;2 from *Arabidopsis thaliana*.

Claim 6 (currently amended): Method according to ~~any one of claims 1 to 4~~ claim 5, wherein said B-type CDK is a class 2 B-type CDK, preferably a CDK B2;2 from *Arabidopsis thaliana*.

Claim 7 (original): Method according to claim 5, wherein said CDK B1;1 nucleic acid is as represented by SEQ ID NO: 1 or by a portion thereof, or by a nucleic acid sequence capable of hybridising therewith, and wherein the CDK B1;1 protein is as represented by SEQ ID NO: 2, or a homologue, derivative or active fragment thereof.

Claim 8 (original): Method according to claim 5, wherein said CDK B1;2 nucleic acid is as represented by SEQ ID NO: 3 or by a portion thereof, or by a nucleic acid sequence capable of hybridising therewith, and wherein the CDK B1;2 protein is as represented by SEQ ID NO: 4, or a homologue, derivative or active fragment thereof.

Claim 9 (original): Method according to claim 6, wherein said CDK B2;2 nucleic acid is as represented by SEQ ID NO: 5 or by a portion thereof, or by a nucleic acid sequence capable of hybridising therewith, and wherein the CDK B2;2 protein is as represented by SEQ ID NO: 6, or a homologue, derivative or active fragment thereof.

Claim 10 (currently amended): Method according to ~~any of claims 1 to 9~~ claim 4, wherein said B-type CDK is a variant nucleic acid or variant amino acids selected from:

- (a) Functional portions of a B-type CDK nucleic acid/gene;
- (b) Sequences capable of hybridising to a B-type CDK nucleic acid/gene;
- (c) Alternative splice variants of a B-type CDK nucleic acid/gene;
- (d) Allelic variants of a B-type CDK nucleic acid/gene;
- (e) Homologues, derivatives and active fragments of a B-type CDK protein;
- (f) Mutant B-type CDKs;

Claim 11 (currently amended): Method according to ~~any one of claim[[s]] 5 to 10~~, wherein expression of said CDK B1;1 nucleic acid is driven by a promoter active in young, expanding tissue, preferably wherein said promoter is a beta expansin promoter.

Claim 12 (currently amended): Method according to ~~any one of claim[[s]] 5 to 10~~, wherein expression of said CDK B1;2 nucleic acid and wherein expression of said CDK B2;2 nucleic acid is driven by a constitutive promoter, preferably wherein said promoter is a GOS 2 promoter.

Claim 13 (currently amended): Method according to ~~any one of claim[[s]] 1 to 12~~, wherein said increased yield comprises one or more of: an increase in area, an increase in the number of panicles, an increase in height, an increase in the number of seeds, an increase in the number of filled seeds, an increase in the total weight of seeds, an increase in thousand kernel weight (TKW) and an increase in harvest index, each relative to control plants.

Claim 14 (currently amended): Method according to ~~any one of claim[[s]] 1 to 13~~, wherein said modified architecture includes one or more of: increase in aboveground area, increase in the number of panicles and an increase in height.

Claim 15 (currently amended): Plants obtainable by a method according to ~~any of claim[[s]] 6 to 14~~.

Claim 16 (original): Construct comprising:

- (a) a B-type CDK gene/nucleic acid encoding a B-type CDK protein; or

- (b) a nucleic acid encoding a CDK mutant, which CDK mutant comprises at least one of the seven amino acid position changes shown in Table A or at least one of the eight amino acid position changes shown in Table B;
- (c) one or more control sequences capable of driving expression of the nucleic acid of (a) or (b); and optionally
- (d) a transcription termination sequence.

Claim 17 (original): Construct according to claim 16, wherein said nucleic acid of (a) is a CDK B1;2 nucleic acid as represented by SEQ ID NO: 3 or by a portion thereof, or by a nucleic acid sequence capable of hybridising therewith, which nucleic acid encodes a CDK B1;2 protein as represented by SEQ ID NO: 4, or a homologue, derivative or active fragment thereof.

Claim 18 (original): Construct according to claim 16, wherein said nucleic acid of (a) is a CDK B2;2 nucleic acid as represented by SEQ ID NO: 5 or by a portion thereof, or by a nucleic acid sequence capable of hybridising therewith, which nucleic acid encodes a CDK B2;2 protein as represented by SEQ ID NO: 6, or a homologue, derivative or active fragment thereof.

Claim 19 (currently amended): Construct according to ~~any one of claim~~[[s]] 16 to 18, wherein said control sequence comprises a constitutive promoter, preferably a GOS 2 promoter.

Claim 20 (original): Method for the production of a transgenic plant having improved growth characteristics selected from any one or more of: increased yield, increased growth rate and modified architecture, which growth characteristics are improved relative to growth characteristics of corresponding wild type plants, said method comprising the steps of:

- (a) introducing into a plant or a plant cell a B-type CDK gene/nucleic; or

- (b) a nucleic acid encoding a CDK mutant, which CDK mutant comprises at least one of the seven amino acid position changes shown in Table A;
- (c) cultivating the plant cell under conditions promoting regeneration and mature plant growth.

Claim 21 (original): Transgenic plant having improved growth characteristics selected from any one or more of: increased yield, increased growth rate and modified architecture, characterised in that said plant has increased expression of a B-type CDK nucleic acid and/or increased activity and/or levels in a plant of a B-type CDK protein relative to corresponding wild type plants.

Claim 22 (original): Transgenic plant according to claim 21, wherein said plant is a monocotyledonous plant.

Claim 23 (canceled).

Claim 24 (original): A composition comprising a protein represented by SEQ ID NO 2, SEQ ID NO: 4 or SEQ ID NO: 6 or a homologue, derivative, or active fragment of any of the aforementioned sequences, for use as a growth regulator.

Claim 25 (original): Screening method for the identification of mutant plant cyclin dependent kinases (CDKs) having enhanced CDK activity relative to corresponding non-mutated plant CDKs, which method comprises the steps of:

- (a) Providing plant-derived CDK mutants;
- (b) Identifying cyclin dependent kinase inhibitor (ICK) non-reacting mutants;
- (c) Identifying mutants having cyclin-binding activity; and optionally followed by,

(d) A yeast complementation assay on resultant mutants from steps (b) and (c).

Claim 26 (original): Screening method for the identification of substantially non-active plant CDKs, but which are capable of binding to plant ICKs, comprising the steps of:

- (a) Providing plant-derived CDK mutants;
- (b) Identifying plant-derived ICK binding mutants; and
- (c) Identifying non-cyclin-binding mutants.

Claim 27 (original): Screening method according to claim 25 or 26 wherein said CDK mutants are provided by the steps of:

- (a) Providing a wild-type Plant CDK; and
- (b) Mutating said CDK at least at 1 amino-acid position;

Claim 28 (currently amended): Mutant CDKs obtainable by the method according to claim ~~25 or~~ 27, which mutant CDKs are indicated in Table A.

Claim 29 (currently amended): Mutant CDKs obtainable by the method according to claim ~~26 or~~ 27, which mutant CDKs are indicated in Table B.

Claim 30 (original): An isolated nucleic acid molecule comprising:

- (a) a nucleic acid encoding a CDK mutant represented by any one of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12 and SEQ ID NO: 13;
- (b) a nucleic acid encoding a homologue, derivative or active fragment of a CDK mutant represented by any one of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12 and SEQ ID NO: 13, which homologue, derivative or active fragment comprises at

- least one of the seven amino acid position changes shown in Table A or at least one of the eight amino acid position changes shown in Table B;
- (c) a nucleic acid capable of hybridising with a nucleic acid of (a) or (b) above, wherein the hybridising sequence encodes an amino acid comprising at least one of the seven amino acid position changes shown in Table A or at least one of the eight amino acid position changes shown in Table B;
 - (d) a nucleic acid of (a) to (c) above which is degenerate as a result of the genetic code;
 - (e) allelic variants of the nucleic acids of (a) to (d), which allelic variant encodes an amino acid comprising at least one of the seven amino acid position changes shown in Table A or at least one of the eight amino acid position changes shown in Table B; and
 - (f) alternative splice variants of the nucleic acids of (a) to (e), which alternative splice variants encode an amino acid comprising at least one of the seven amino acid position changes shown in Table A or at least one of the eight amino acid position changes shown in Table B.

Claim 31 (original): A CDK mutant, comprising:

- (a) an amino acid represented by any one of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12 and SEQ ID NO: 13; and
- (b) a fragment of an amino acid represented by any one of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12 and SEQ ID NO: 13, which fragment comprises at least seven amino acid position changes shown in Table A or at least one of the eight amino acid position changes shown in Table B.